What is claimed is:

1. A method for gene diagnosis of bovine Hsp70 deficiency, which comprises the following steps,

(a) a step of obtaining a bovine nucleic acid sample,

(b) a step of subjecting the nucleic acid sample obtained in step (a) to a gene amplification reaction to obtain a nucleic acid fragment in which a region including a mutation site likely to be present in bovine Hsp70 gene is amplified, and

(c) a step of examining the presence of mutation on the nucleic acid fragment in step (b),

the region including the mutation site being a region including 1997-11030 position of a base sequence shown in SEQ ID No. 1 of SEQUENCE LISTING in a base sequence of bovine Hsp70 gene.

2. The method for gene diagnosis as claimed in claim 1, wherein the gene amplification reaction is conducted by a polymerase chain reaction method.

3. The method for gene diagnosis as claimed in claim 1 or 2, wherein the presence of mutation is examined by examining a gene amplification product obtained by the polymerase chain reaction method.

4. The method for gene diagnosis as claimed in any one of claims 1 to 3, wherein the nucleic acid sample is a sample containing genomic DNA, cDNA or mRNA.

5. A method for gene diagnosis of bovine Hsp70 deficiency, which comprises conducting genome linkage analysis of subject bovine, isolating bovine Hsp70 gene by positional cloning, determining a base sequence of the gene by a usual manner, and examining the presence or absence of mutation by comparing said base sequence with a base sequence of cDNA encoding normal bovine Hsp70 as shown in SEQ ID No. 1 of SEQUENCE LISTING.

6. A kit for detecting bovine Hsp70 deficiency, which kit contains oligonucleotide primers used for amplifying a region including a mutation site likely to be present in bovine Hsp70 gene by a gene amplification reaction, the oligonucleotide primers being selected from the group consisting of

(1) oligonucleotides having a base sequence corresponding to a 5'-terminal region in a base sequence shown in SEQ ID No. 1 of SEQUENCE LISTING, and

(2) oligonucleotides having a complementary base sequence to a 3'-terminal region in the base sequence shown in SEQ ID No. 1 of SEQUENCE LISTING.

7. The kit as claimed in claim 6, wherein the oligonucleotide primers comprise from 15 to 35 nucleotides.

8. The kit as claimed in claim 6, wherein the oligonucleotide primers are a pair of oligonucleotide primers selected from the group consisting of those shown in SEQ ID

Nos. 2 to 8 of SEQUENCE LISTING, provided combinations of SEQ ID Nos. 2 and 4, 3 and 5, and 6 and 7 are excluded.